

R Studio Code for PCA, Pearson correlations & heat map generation

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## Principal Components Analysis (PCA) using the stats package prcomp function
## Heatmap generation using the NMF package aheatmap function
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#load packages if not already loaded
library(stats)

#use read.table function to pull in csv file containing the Z-scores for your signaling data

dat0=read.table("your_Zscores.csv", header= TRUE, sep=";")
dat1=dat0[,2:ncol(dat0)]
rownames(dat1)=dat0$sample

# create correlation heatmaps
# for samples (serum lots) & features (serum components)
install.packages("NMF")
library(NMF)

cor_samples = cor(dat1)
cor_features = cor(t(dat1))

aheatmap(cor_samples,breaks=c(0),revC=T, filename ='cor_samples2.pdf')
aheatmap(cor_features,breaks=c(0),revC=T, filename ='cor_features2.pdf')

# PCA using prcomp
pcamat <- t(dat1)
pcadat <- prcomp(pcamat,center=T,scale=T,retx=T)

#pcamat is the matrix that contains z scores
# the transform is take here to have samples as rows and msmts as columns
# center is a logical value indicating whether the variables should be shifted or zero centered
# scale is a logical value indicating whether the variables should be scaled to have unit variance
#retx is a logical value indicating whether the rotated variables should be returned

# scores
sc <- pcadat$x
#loadings
ld <- pcadat$rotation

# scree plot and variance capture
screeplot(pcadat)
eigVals = (pcadat$sdev)^2
varExp <- eigVals*100/sum(eigVals)

# scores and loadings biplot
biplot(pcadat, filename ='biplot.pdf')

#Export tables with scores and loadings using write.table function
write.table(sc, file="scores.txt",col.names=T,row.names=T,sep="\t", quote=F)
write.table(ld, file="loadings.txt",col.names=T,row.names=T,sep="\t", quote=F)
write.table(varExp, file="variance.txt",col.names=T,row.names=T,sep="\t", quote=F)

#exported scores and loadings can be used be plotted with software of choice, eg. Kaleidograph
```